

Output tables for 1xN statistical comparisons.

December 17, 2022

1 Average rankings of Friedman Alligned test

Average ranks obtained by each method in the Friedman Alligned test.

Algorithm	Ranking
MEABC	155.3793
ABCADE	98.3103
ABCNG	125.0345
SHADE	80.569
MAPSO	109.6552
TAPSO	79.4483
MEEABC	65.6034

Table 1: Average Rankings of the algorithms (Aligned Friedman)

Aligned Friedman statistic (distributed according to chi-square with 6 degrees of freedom): 24.496317.
P-value computed by Aligned Friedman Test: 0.000423097865.

2 Post hoc comparison (Friedman Alligned)

P-values obtained in by applying post hoc methods over the results of Friedman Alligned procedure.

i	algorithm	$z = (R_0 - R_i)/SE$	p	Holm	Hochberg	Hommel	Holland	Rom
6	ME/ABC	5.819305	0			0.008333	0.008512	0.008764
5	ABCNG	3.852342	0.000117			0.01	0.010206	0.010515
4	MAPSO	2.855449	0.004298			0.0125	0.012741	0.013109
3	ABCADE	2.120073	0.034			0.016667	0.016952	0.016667
2	SHADE	0.97007	0.332011			0.025	0.025321	0.025
1	TAPSO	0.897427	0.369491			0.05	0.05	0.05

Table 2: Post Hoc comparison Table for $\alpha = 0.05$ (FRIEDMAN ALLIGNED)

Bonferromi-Dunn's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.008333 .
Holm's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.016667 .
Hochberg's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.0125 .
Hommel's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.016667 .
Holland's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.016952 .
Rom's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.013109 .

3 Adjusted P-Values (Friedman Aligned)

Adjusted P-values obtained through the application of the post hoc methods (Friedman Aligned).

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	$p_{Hochberg}$	p_{Hommel}
1	MEABC	0	0	0	0	0
2	ABCNG	0.000117	0.000702	0.000585	0.000585	0.000585
3	MAPSO	0.004298	0.025786	0.01719	0.01719	0.01719
4	ABCADE	0.034	0.203999	0.102	0.102	0.102
5	SHADE	0.332011	1.992068	0.664023	0.369491	0.369491
6	TAPSO	0.369491	2.216947	0.664023	0.369491	0.369491

Table 3: Adjusted p -values (ALIGNED FRIEDMAN) (I)

i	algorithm	unadjusted p	$p_{Holland}$	p_{Rom}
1	MEABC	0	0	0
2	ABCNG	0.000117	0.000585	0.000556
3	MAPSO	0.004298	0.01708	0.016391
4	ABCADE	0.034	0.098571	0.102
5	SHADE	0.332011	0.553791	0.369491
6	TAPSO	0.369491	0.553791	0.369491

Table 4: Adjusted p -values (ALIGNED FRIEDMAN) (II)